Access DB# 146189

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 2/25/05
Art Unit: 1636 Phone Number ~~30~~ 272-0767 Serial Number: 10/613106
Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please run a regular plus interference sequence search on SEQ ID NO: 1 and 4.

CRFE

1 - NA - 986

4 - NA - 2144

Thanks

MEJ

Amended 2-2532
3/7/05 - 3/9/05

****

STAFF USE ONLY | **Type of Search** | **Vendors and cost where applicable**

Searcher: | NA Sequence (#) | STN

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 8, 2005, 13:21:02 ; Search time 4143.41 Seconds
(without alignments)
11530.816 Million cell updates/sec

Title: US-10-613-106-1
Perfect score: 986
Sequence: 1 atgagacatattatctgcca.....gtaaacgccccaggccataa 986

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	986	100.0	1000	6	AR016484	AR016484 Sequence
2	986	100.0	1000	6	AR016485	AR016485 Sequence
3	986	100.0	1000	6	AR031949	AR031949 Sequence
4	986	100.0	1000	6	AR031950	AR031950 Sequence
5	986	100.0	1000	6	I20734	I20734 Sequence 1
6	986	100.0	1000	6	I20735	I20735 Sequence 3
7	986	100.0	1000	6	AR304631	AR304631 Sequence
8	986	100.0	1000	6	AR304632	AR304632 Sequence
9	986	100.0	1055	14	AY147066	AY147066 Human ade
10	986	100.0	1802	6	AX817767	AX817767 Sequence
11	986	100.0	1802	6	AX838364	AX838364 Sequence
12	986	100.0	3408	6	AX770195	AX770195 Sequence
13	986	100.0	7090	6	AR310582	AR310582 Sequence
14	986	100.0	7090	6	AX150263	AX150263 Sequence
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17	986	100.0	11152	6	AX356041	AX356041 Sequence
18	986	100.0	11152	6	BD021940	BD021940 Packaging
19	986	100.0	11570	14	AD5001	X02996 Adenovirus
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25	986	100.0	32802	6	CQ854906	CQ854906 Sequence
26	986	100.0	33699	6	AX084506	AX084506 Sequence
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ALIGNMENTS

RESULT 1
AR016484
LOCUS AR016484 1000 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 1 from patent US 5776743.
ACCESSION AR016484
VERSION AR016484.1 GI:3972761
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1000)
AUTHORS Frisch,S.M.
TITLE Method of sensitizing tumor cells with adenovirus E1A
JOURNAL Patent: US 5776743-A 1 07-JUL-1998;
FEATURES Location/Qualifiers
source 1. .1000
/organism="unknown"
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ORIGIN

Query Match 100.0%; Score 986; DB 6; Length 1000;
Best Local Similarity 100.0%; Pred. No. 1e-263;
Matches 986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db        190 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 249

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
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Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
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Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
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Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
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Db        910 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 969

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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Db        970 TGAGCTGTAAACGCCCCAGGCCATAA 995


RESULT 2
AR016485
LOCUS       AR016485                1000 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 3 from patent US 5776743.
ACCESSION   AR016485
VERSION     AR016485.1  GI:3972762
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Frisch,S.M.
  TITLE     Method of sensitizing tumor cells with adenovirus E1A
  JOURNAL   Patent: US 5776743-A 3 07-JUL-1998;
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1e-263;

  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
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Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Db        430 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 489

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Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
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Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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RESULT 3
AR031949
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LOCUS       AR031949               1000 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5866550.
ACCESSION   AR031949
VERSION     AR031949.1  GI:5946238
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Frisch,S.M.
  TITLE     Method of inhibiting replication of hyperproliferative cells using
            a nucleic acid encoding EIA
  JOURNAL   Patent: US 5866550-A 1 02-FEB-1999;
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
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Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
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Db        370 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 429

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Db        430 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 489

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
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Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
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Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 4
AR031950
LOCUS       AR031950               1000 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 3 from patent US 5866550.
ACCESSION   AR031950
VERSION     AR031950.1  GI:5946239
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SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Frisch,S.M.
  TITLE     Method of inhibiting replication of hyperproliferative cells using
            a nucleic acid encoding EIA
  JOURNAL   Patent: US 5866550-A 3 02-FEB-1999;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 986;  DB 6;  Length 1000;
  Best Local Similarity   100.0%;  Pred. No. 1e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 69

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 129

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
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Db        130 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 189

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
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Db        190 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 249

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 309

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
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Db        310 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 369

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
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Db        370 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 429

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Db        430 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 489

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540

Db        490 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 549

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600

Db        550 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 609

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660

Db        610 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 669

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720

Db        670 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 729

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780

Db        730 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 789

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840

Db        790 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 849

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900

Db        850 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 909

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960

Db        910 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 969

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986

Db        970 TGAGCTGTAAACGCCCCAGGCCATAA 995


RESULT 5
I20734
LOCUS       I20734                  1000 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 1 from patent US 5516631.
ACCESSION   I20734
VERSION     I20734.1  GI:1601089
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Frisch,S.M.
  TITLE     Method of inhibiting replication of hyperproliferative cells
  JOURNAL   Patent: US 5516631-A 1 14-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .1000
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           100.0%;  Score 986;  DB 6;  Length 1000;
  Best Local Similarity  100.0%;  Pred. No. 1e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60

Db         10 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 69

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120

Db         70 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 129

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180

Db        130 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 189

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240

Db        190 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 249

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300

Db        250 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 309

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360

Db        310 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 369

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420

Db        370 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 429

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480

Db        430 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 489

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540

Db        490 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 549

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600

Db        550 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 609

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660

Db        610 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 669

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720

Db        670 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 729

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780

Db        730 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 789

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840

Db        790 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 849

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900

Db        850 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 909

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960

Db        910 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 969

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986

Db        970 TGAGCTGTAAACGCCCCAGGCCATAA 995


RESULT 6
I20735
LOCUS       I20735                  1000 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 3 from patent US 5516631.
ACCESSION   I20735
VERSION     I20735.1  GI:1601090
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Frisch,S.M.
  TITLE     Method of inhibiting replication of hyperproliferative cells
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  JOURNAL   Patent: US 5516631-A 3 14-MAY-1996;
FEATURES             Location/Qualifiers
     source          1. .1000
                     /organism="unknown"
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ORIGIN

  Query Match           100.0%;  Score 986;  DB 6;  Length 1000;
  Best Local Similarity  100.0%;  Pred. No. 1e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Db         10 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 69

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
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Db         70 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 129

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 189

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
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Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
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Db        250 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 309

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
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Db        310 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 369

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
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Db        370 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 429

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
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Db        490 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 549

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        550 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 609

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
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Db        610 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 669

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
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Db        670 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 729

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Db        730 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 789

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        790 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 849

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
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Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        910 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 969

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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Db        970 TGAGCTGTAAACGCCCCAGGCCATAA 995


RESULT 7
AR304631
LOCUS       AR304631                1000 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 1 from patent US 6544955.
ACCESSION   AR304631
VERSION     AR304631.1  GI:31693815
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Frisch,S.M.
  TITLE     Method of sensitizing tumor cells with adenovirus E1A
  JOURNAL   Patent: US 6544955-A 1 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .1000
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ORIGIN

  Query Match           100.0%;  Score 986;  DB 6;  Length 1000;
  Best Local Similarity  100.0%;  Pred. No. 1e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 69

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
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Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
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Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
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Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
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Db        370 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 429

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
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Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
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Db        610 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 669

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
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Db        670 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 729

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
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Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
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Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
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Db        910 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 969

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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Db        970 TGAGCTGTAAACGCCCCAGGCCATAA 995


RESULT 8
AR304632
LOCUS       AR304632                1000 bp    mRNA    linear   PAT 12-JUN-2003
DEFINITION  Sequence 3 from patent US 6544955.
ACCESSION   AR304632
VERSION     AR304632.1  GI:31693816
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1000)
  AUTHORS   Frisch,S.M.
  TITLE     Method of sensitizing tumor cells with adenovirus E1A
  JOURNAL   Patent: US 6544955-A 3 08-APR-2003;
FEATURES             Location/Qualifiers
     source          1. .1000
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ORIGIN

  Query Match           100.0%;  Score 986;  DB 6;  Length 1000;
  Best Local Similarity  100.0%;  Pred. No. 1e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Db         10 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 69

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
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Db         70 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 129

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
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Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
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Db        310 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 369

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
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Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
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Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
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Db        550 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 609

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 669

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 729

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 789

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
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Db        790 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 849

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        850 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 909

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 969

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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Db        970 TGAGCTGTAAACGCCCCAGGCCATAA 995


RESULT 9
AY147066
LOCUS       AY147066                1055 bp    DNA     linear   VRL 16-SEP-2002
DEFINITION  Human adenovirus type 5 E1A protein gene, complete cds.
ACCESSION   AY147066
VERSION     AY147066.1  GI:22947855
KEYWORDS    .
SOURCE      Human adenovirus type 5
  ORGANISM  Human adenovirus type 5
            Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE   1  (bases 1 to 1055)
  AUTHORS   Li,L., Wang,Z., Su,M., Yu,W. and Ma,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-2002) Institute of Orthopaedics, XiJing Hospital,
            17# ChangLe West Road, Xi'an, Shaanxi 710032, P.R. China
FEATURES             Location/Qualifiers
     source          1. .1055
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:28285"
     CDS             join(44. .596,713. .1029)
                     /codon_start=1
                     /product="E1A protein"
                     /protein_id="AAN08102.1"
                     /db_xref="GI:22947856"
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RRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPEPEPEPEPARPTRRPKMAPAILRRPT
SPVSRECNSSTDSCDSGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDLLNEP
GQPLDLSCKRPRP"

ORIGIN

Query Match 100.0%; Score 986; DB 14; Length 1055;
Best Local Similarity 100.0%; Pred. No. 1e-263;
Matches 986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Db         44 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 103

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
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Db        104 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 163

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
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Db        164 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 223

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
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Db        224 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 283

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
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Db        284 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 343

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 403

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
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Db        404 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 463

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Db        464 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 523

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
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Db        524 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 583

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
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Db        584 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 643

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 703

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
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Db        704 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 763

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
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Db        764 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 823

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
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Db        824 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 883

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 943

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
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Db        944 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 1003

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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Db       1004 TGAGCTGTAAACGCCCCAGGCCATAA 1029
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RESULT 10
AX817767
LOCUS AX817767 1802 bp DNA linear PAT 10-DEC-2003
DEFINITION Sequence 3 from Patent WO02067861.
ACCESSION AX817767
VERSION AX817767.1 GI:39722964
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS .
TITLE Oncolytic adenoviral vectors
JOURNAL Patent: WO 02067861-A 3 06-SEP-2002;
FEATURES Location/Qualifiers
source 1. .1802
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/note="viral vector construct"
misc_feature 1. .1802
/note="Fig. 3 A-Left end of Ar6pAE2fF sequence"

ORIGIN

Query Match 100.0%; Score 986; DB 6; Length 1802;
Best Local Similarity 100.0%; Pred. No. 1.1e-263;
Matches 986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Db        582 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 641

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 701

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 761

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 821

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 881

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 941

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 1001

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Db       1002 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 1061

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
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Db       1062 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 1121

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
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Db       1122 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 1181

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
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Db       1182 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 1241

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1242 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 1301

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1302 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 1361

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
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Db       1362 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 1421

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
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Db       1422 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 1481

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
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Db       1482 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 1541

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
              |||||||||||||||||||||||||
Db       1542 TGAGCTGTAAACGCCCCAGGCCATAA 1567
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RESULT 11
AX838364
LOCUS AX838364 1802 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 3 from Patent WO02068627.
ACCESSION AX838364
VERSION AX838364.1 GI:39922045
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS .
TITLE Vector constructs
JOURNAL Patent: WO 02068627-A 3 06-SEP-2002;
FEATURES Location/Qualifiers
source 1. .1802
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="viral vector construct"
misc_feature 1. .1802
/note="Fig. 3 A - left end of Ar6pAE2fF sequence"
ORIGIN

Query Match 100.0%; Score 986; DB 6; Length 1802;
Best Local Similarity 100.0%; Pred. No. 1.1e-263;
Matches 986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Db        582 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 641

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
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Db        642 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 701

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 761

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
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Db        762 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 821

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
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Db        822 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 881

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 941

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 1001

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
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Db       1002 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 1061

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1062 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 1121

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1122 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 1181

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1182 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 1241

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
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Db       1242 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 1301

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
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Db       1302 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 1361

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
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Db       1362 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 1421

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1422 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 1481

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
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Db       1482 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 1541

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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Db       1542 TGAGCTGTAAACGCCCCAGGCCATAA 1567
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RESULT 12
AX770195
LOCUS AX770195 3408 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 6 from Patent WO03035883.
ACCESSION AX770195
VERSION AX770195.1 GI:32437735
KEYWORDS .
SOURCE Human adenovirus type 5
ORGANISM Human adenovirus type 5
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
REFERENCE 1
AUTHORS Hochberg,A. and Ayesh,S.
TITLE Methods and compositions for inducing tumor-specific cytotoxicity
JOURNAL Patent: WO 03035883-A 6 01-MAY-2003;
Yissum Research and Development Co. of the Hebrew Univ of Jerusalem (IL)
FEATURES Location/Qualifiers
source 1. .3408

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                     /db_xref="GI:32437736"
                     /translation="MRHIICHGGVITEEMAASLLDQLIEEVLADNLPPPSHFEPPTLH
                     ELYDLDVTAPEDPNEEAVSQIFPDSVMLAVQEGIDLLTFPPAPGSPEPPHLSRQPEQP
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                     RRNTGDPDIMCSLCYMRTCGMFVYSPVSEPEPEPEPEPARPTRRPKMAPAILRRPT
                     SPVSRECNSSTDSCDSGPSNTPPEIHPVVPLCPIKPVAVRVGGRRQAVECIEDLLNEP
                     GQPLDLSCKRPRP"
ORIGIN

  Query Match             100.0%;  Score 986;  DB 6;  Length 3408;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Db         44 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 103

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 163

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        164 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 223

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 283

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
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Db        284 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 343

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 403

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 463

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 523

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 583

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        584 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 643

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        644 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 703

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        704 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 763

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        764 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 823

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        824 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 883

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        884 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 943

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        944 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 1003

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
              |||||||||||||||||||||||||
Db       1004 TGAGCTGTAAACGCCCCAGGCCATAA 1029


RESULT 13
AR310582
LOCUS       AR310582               7090 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 18 from patent US 6558948.
ACCESSION   AR310582
VERSION     AR310582.1  GI:31703596
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 7090)
  AUTHORS   Kochanek,S. and Schiedner,G.
  TITLE     Permanent amniocytic cell line, its production and use for the
            production of gene transfer vectors
  JOURNAL   Patent: US 6558948-A 18 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .7090
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 986;  DB 6;  Length 7090;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 2867

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2868 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 2927

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2928 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 2987

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
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Db       2988 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 3047

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3048 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 3107

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3108 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 3167

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3168 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 3227

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3228 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 3287
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Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3288 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 3347

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3348 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 3407

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3408 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 3467

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3468 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 3527

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
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Db       3528 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 3587

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3588 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 3647

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3648 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 3707

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3708 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 3767

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
              |||||||||||||||||||||||||
Db       3768 TGAGCTGTAAACGCCCCAGGCCATAA 3793
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RESULT 14
AX150263
LOCUS AX150263 7090 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 18 from Patent WO0136615.
ACCESSION AX150263
VERSION AX150263.1 GI:14348283
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Kochanek,S. and Schiedner,G.
TITLE Permanent amniocyte cell line, the production thereof and its use for producing gene transfer vectors
JOURNAL Patent: WO 0136615-A 18 25-MAY-2001;
Kochanek, Stefan (DE)
FEATURES Location/Qualifiers
source 1. .7090
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Plasmid STK146"
ORIGIN

Query Match 100.0%; Score 986; DB 6; Length 7090;
Best Local Similarity 100.0%; Pred. No. 1.5e-263;
Matches 986; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2808 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 2867

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2868 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 2927
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Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2928 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 2987

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2988 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 3047

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3048 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 3107

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3108 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 3167

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3168 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 3227

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3228 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 3287

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3288 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 3347

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3348 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 3407

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3408 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 3467

Qy        661 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3468 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 3527

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3528 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 3587

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3588 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 3647

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3648 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 3707

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
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Db       3708 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 3767

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
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Db       3768 TGAGCTGTAAACGCCCCAGGCCATAA 3793
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RESULT 15
BD268237
LOCUS BD268237 7607 bp DNA linear PAT 17-JUL-2003
DEFINITION Adenovirus vector, packaging cell line, composition and method for production and use.
ACCESSION BD268237
VERSION BD268237.1 GI:33078005
KEYWORDS JP 2002534130-A/41.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 7607)

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  AUTHORS   Nemerow,G.R., Seggern,D.J.V., Hallenbeck,P.L., Stevenson,S.C. and
            Skripchenko,Y.
  TITLE     Adenovirus vector, packaging cell line, composition and method for
            production and use
  JOURNAL   Patent: JP 2002534130-A 41 15-OCT-2002;
            NOVARTIS AG,THE SCRIPPS RESEARCH INSTITUTE
COMMENT     OS   Artificial Sequence
            PN   JP 2002534130-A/41
            PD   15-OCT-2002
            PF   14-JAN-2000 JP 2000593765
            PR   14-JAN-1999 US    60/115920
            PI   GLEN ROBERT NEMEROW,DANIEL J VON SEGGERN,PAUL L HALLENBECK, PI
              SUSAN C STEVENSON,YELENA SKRIPCHENKO
            PC   C12N15/09,A61K35/76,A61K48/00,A61P35/00,A61P43/00,A61P43/00,
            PC   C12N5/10,
            PC   C12N7/00,C12Q1/68,G01N33/53,G01N33/566,C12N15/00,C12N5/00 CC
            Description of Artificial Sequence: plasmid
            FH   Key             Location/Qualifiers
            FT   source          1. .7607
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .7607
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ORIGIN

  Query Match           100.0%;  Score 986;  DB 6;  Length 7607;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-263;
  Matches  986;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 60
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Db        977 ATGAGACATATTATCTGCCACGGAGGTGTTATTACCGAAGAAATGGCCGCCAGTCTTTTG 1036

Qy         61 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1037 GACCAGCTGATCGAAGAGGTACTGGCTGATAATCTTCCACCTCCTAGCCATTTTGAACCA 1096

Qy        121 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1097 CCTACCCTTCACGAACTGTATGATTTAGACGTGACGGCCCCCGAAGATCCCAACGAGGAG 1156

Qy        181 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 240
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Db       1157 GCGGTTTCGCAGATTTTTCCCGACTCTGTAATGTTGGCGGTGCAGGAAGGGATTGACTTA 1216

Qy        241 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 300
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Db       1217 CTCACTTTTCCGCCGGCGCCCGGTTCTCCGGAGCCGCCTCACCTTTCCCGGCAGCCCGAG 1276

Qy        301 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 360
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Db       1277 CAGCCGGAGCAGAGAGCCTTGGGTCCGGTTTCTATGCCAAACCTTGTACCGGAGGTGATC 1336

Qy        361 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 420
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Db       1337 GATCTTACCTGCCACGAGGCTGGCTTTCCACCCAGTGACGACGAGGATGAAGAGGGTGAG 1396

Qy        421 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1397 GAGTTTGTGTTAGATTATGTGGAGCACCCCGGGCACGGTTGCAGGTCTTGTCATTATCAC 1456

Qy        481 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 540
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Db       1457 CGGAGGAATACGGGGGACCCAGATATTATGTGTTCGCTTTGCTATATGAGGACCTGTGGC 1516

Qy        541 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 600
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Db       1517 ATGTTTGTCTACAGTAAGTGAAAATTATGGGCAGTGGGTGATAGAGTGGTGGGTTTGGTG 1576

Qy        601 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 660
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Db       1577 TGGTAATTTTTTTTTTAATTTTTACAGTTTTGTGGTTTAAAGAATTTTGTATTGTGATTT 1636

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Db       1637 TTTTAAAAGGTCCTGTGTCTGAACCTGAGCCTGAGCCCGAGCCAGAACCGGAGCCTGCAA 1696

Qy        721 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 780
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Db       1697 GACCTACCCGCCGTCCTAAAATGGCGCCTGCTATCCTGAGACGCCCGACATCACCTGTGT 1756

Qy        781 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 840
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Db       1757 CTAGAGAATGCAATAGTAGTACGGATAGCTGTGACTCCGGTCCTTCTAACACACCTCCTG 1816

Qy        841 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1817 AGATACACCCGGTGGTCCCGCTGTGCCCCATTAAACCAGTTGCCGTGAGAGTTGGTGGGC 1876

Qy        901 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1877 GTCGCCAGGCTGTGGAATGTATCGAGGACTTGCTTAACGAGCCTGGGCAACCTTTGGACT 1936

Qy        961 TGAGCTGTAAACGCCCCAGGCCATAA 986
              |||||||||||||||||||||||||
Db       1937 TGAGCTGTAAACGCCCCAGGCCATAA 1962


Search completed: March  8, 2005, 23:38:35
Job time : 4147.41 secs
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